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OM nucleic - nucleic search, using sw model

Run on: May 9, 2002, 21:30:48 ; Search time 1941.08 Seconds
(without alignments)
2425.696 Million cell updates/sec

Title: US-08-037-230D-18

Perfect score: 225

Sequence: 1 TATTCTTCTGTCATCTT.....CGGACTGTCCTGAGGAG 225

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

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14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

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22: em.ov.*

23: em.pat.*

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25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg_hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	225	100.0	225	6	AR153509	AR153509 Sequence	
2	225	100.0	225	6	I36933	I36933 Sequence 18	
3	157	69.8	945	6	AR167371	AR167371 Sequence	
4	157	69.8	945	6	HSU10339	U10339 Human MAGE-	
5	157	69.8	1019	6	AR167377	AR167377 Sequence	
6	157	69.8	1019	9	HUMMAGEB	D32076 Human mRNA	
7	157	69.8	1362	6	AX019384	AX019384 Sequence	
8	157	69.8	3871	9	HSU10691	U10691 Human MAGE-	
9	157	69.8	245077	9	AF002997	AF002997 Homo sapi	
10	74	32.9	1212	6	AX019380	AX019380 Sequence	
11	74	32.9	1353	6	AX019376	AX019376 Sequence	
12	74	32.9	1569	6	AX343855	AX343855 Sequence	
13	74	32.9	1640	6	AR153502	AR153502 Sequence	
14	74	32.9	1640	6	I36926	I36926 Sequence 11	
15	74	32.9	1663	9	BC011744	BC011744 Homo sapi	
16	74	32.9	1709	9	BC000340	BC000340 Homo sapi	
17	74	32.9	1710	9	BC017389	BC017389 Homo sapi	
18	74	32.9	1715	9	BC016803	BC016803 Homo sapi	
19	74	32.9	1753	9	BC005963	BC005963 Homo sapi	
20	74	32.9	4204	6	AR079453	AR079453 Sequence	
21	74	32.9	4204	6	AR167370	AR167370 Sequence	
22	74	32.9	4204	6	AR170361	AR170361 Sequence	
23	74	32.9	4204	6	AX333265	AX333265 Sequence	
24	74	32.9	4204	9	HSU03735	U03735 Human MAGE-	
c	25	74	32.9	245077	9	AF002997	AF002997 Homo sapi
c	26	74	32.9	289248	9	U82671	U82671 Homo sapien
27	39	17.3	951	9	AF443295	AF443295 Homo sapi	
28	36	16.0	727	6	AX328164	AX328164 Sequence	
29	36	16.0	1657	9	BC013098	BC013098 Homo sapi	
30	36	16.0	1678	9	BC003408	BC003408 Homo sapi	
c	31	36	16.0	3295	2	AC084372	AC084372 Homo sapi
32	36	16.0	4157	6	AR153500	AR153500 Sequence	
33	36	16.0	4157	6	I36924	I36924 Sequence 9	
34	36	16.0	4559	6	AR167369	AR167369 Sequence	
35	36	16.0	4559	9	HUMMAGE2X	HL8920 Human MAGE-	
36	36	16.0	289248	9	U82671	U82671 Homo sapien	
37	36	16.0	302250	6	AX335531	AX335531 Sequence	
c	38	36	16.0	302250	6	AX335531	AX335531 Sequence
39	27	12.0	27	6	I15301	I15301 Sequence 9	
40	27	12.0	27	6	I84649	I84649 Sequence 9	
c	41	26	11.6	26	AR099857	AR099857 Sequence	
42	26	11.6	1030	6	AX328166	AX328166 Sequence	
43	26	11.6	4523	6	AX119704	AX119704 Sequence	
44	26	11.6	4523	9	HUMMAGE12X	HL8877 Human MAGE-	
c	24	10.7	24	6	AR086398	AR086398 Sequence	

ALIGNMENTS

RESULT 1

AR153509

LOCUS

DEFINITION

AR153509

ACCESSION

AR153509.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 225)

AUTHORS

van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.

TITLE

Isolated nucleic acid molecules coding for tumor rejection antigen

precursor MAGE-3 and uses thereof

JOURNAL

Patent: US 6235525-A 18 22-MAY-2001;

FEATURES

Location/Qualifiers

source

1..225

/organism="unknown"

AR153509

Sequence 18 from patent US 6235525.

AR153509

AR153509.1

GI:15121041

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 225)

van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.

Isolated nucleic acid molecules coding for tumor rejection antigen

precursor MAGE-3 and uses thereof

Patent: US 6235525-A 18 22-MAY-2001;

Location/Qualifiers

1..225

/organism="unknown"

44 a

65 c

58 g

58 t

Query Match

100.0%; Score 225; DB 6; Length 225;

Best Local Similarity 100.0%; Pred. No. 6.1e-121;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACAGCTGGTCTTTGGCATC 60
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Db 1 TATTTCCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACAGCTGGTCTTTGGCATC 60
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QY 61 GAGCTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGTCGCCAGGACAGGCTTCCTGATAATC 180
Db 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGTCGCCAGGACAGGCTTCCTGATAATC 180
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QY 181 ATCTTGCCCATATTCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
Db 181 ATCTTGCCCATATTCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
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RESULT 2
LOCUS I36933 225 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 18 from patent US 5612201.
ACCESSION I36933
VERSION I36933.1 GI:2084893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 225)
AUTHORS De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C.
and Chomez,P.
TITLE Isolated nucleic acid molecules useful in determining expression of
a tumor rejection antigen precursor
JOURNAL Patent: US 5612201-A 18 MAR-1997;
FEATURES Location/Qualifiers
source
I. .225
/organism="unknown"
BASE COUNT 44 a 65 c 58 g 58 t
ORIGIN

Query Match 100.0%; Score 225; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.1e-121;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACAGCTGGTCTTTGGCATC 60
Db 1 TATTTCCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACAGCTGGTCTTTGGCATC 60
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QY 61 GAGCTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGTCGCCAGGACAGGCTTCCTGATAATC 180
Db 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGTCGCCAGGACAGGCTTCCTGATAATC 180
|||||

QY 181 ATCTTGCCCATATTCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
Db 181 ATCTTGCCCATATTCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
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RESULT 3
LOCUS AR167371 945 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6287569.
ACCESSION AR167371
VERSION AR167371.1 GI:17903147
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 945)
AUTHORS Kipps,T.J. and Wu,Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 7 II-SEP-2001;
FEATURES Location/Qualifiers
source
I. .945
/organism="unknown"
BASE COUNT 213 a 254 c 275 g 203 t
ORIGIN

Query Match 69.8%; Score 157; DB 6; Length 945;
Best Local Similarity 100.0%; Pred. No. 6.3e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACAGCTGGTCTTTGGCATCGAG 63
Db 436 TTCTTTCTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACAGCTGGTCTTTGGCATCGAG 495
|||||

QY 64 CTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 123
Db 496 CTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTCTCC 555
|||||

QY 124 TAGCATGGCCTGCTGGGTGACAATCAGATCATGCCCCA 160
Db 556 TAGCATGGCCTGCTGGGTGACAATCAGATCATGCCCCA 592
|||||

RESULT 4
LOCUS HSU10339 945 bp mRNA linear PRI 13-JUN-1994
DEFINITION Human MAGE-3b mRNA, complete cds.
ACCESSION U10339
VERSION U10339.1 GI:499121
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Cloning and Analysis of MAGE-1 Related Genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1994) Robert G. Fenton, BRMP, NCI-FCRDC,
Frederick, MD 21702, USA
FEATURES Location/Qualifiers
source
I. .945
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAGE-3b"
/haplotype="HLA-A1/A2"
/cell_line="DM150"
/cell_type="melanoma"
/tissue_type="skin"
/clone_lib="DM150 library"
/dev_stage="adult"
/note="cancer patient"
I. .945
/codon_start=1
/product="MAGE-3b"
/protein_id="AA19006.1"
/db_xref="GI:499122"

CDS
1 (bases 1 to 945)
/translation="MPLEQRSQHKPEEGLEARGEALGLVGAQAPATEQEAAASSST
LVEVTIGEPAAESPDPQSPQAGASLPTTMMYPLMSQSYEDSSNQEESGPFDPLE
SEFOAALSRLKVLKLVHLLKYRAREPVTKAEMIGSVGNWVFFVIFSKASDSLQ
VFQILMEVDPIGHVYIFATCLGLSYDGLLDNQIMPKTGLFLLIIILAIKEDCAPE
EKIWEELSLEVEFEGEDSIFGDPKLLLTQYFQENYLEYRQVPGSDPACYEFLWGR
ALTIETSVKVLHHMKISGGPRISYPLLHWAALREGEE"

BASE COUNT 213 a 254 c 275 g 203 t

ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 945;
Best Local Similarity 100.0%; Pred. No. 6.3e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTCTGATCTTCAGCAAGCTTCGGTGCATCTTCCTTCGAGCTGGTCTTTGGCATCGAG 63
Db 436 TTCTTTCTCTGATCTTCAGCAAGCTTCGGTGCATCTTCCTTCGAGCTGGTCTTTGGCATCGAG 495

QY 64 CTGATGAAGTGCACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 123
Db 496 CTGATGAAGTGCACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 555

QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
Db 556 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 592

RESULT 5
LOCUS AR167377 1019 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6287569.
ACCESSION AR167377
VERSION AR167377.1 GI:17903153
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS Kippes,T.J. and Wu,Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 13 11-SEP-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 224 a 284 c 292 g 219 t
ORIGIN

Query Match 69.8%; Score 157; DB 6; Length 1019;
Best Local Similarity 100.0%; Pred. No. 6.3e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTCTGATCTTCAGCAAGCTTCGGTGCATCTTCCTTCGAGCTGGTCTTTGGCATCGAG 63
Db 501 TTCTTTCTCTGATCTTCAGCAAGCTTCGGTGCATCTTCCTTCGAGCTGGTCTTTGGCATCGAG 560

QY 64 CTGATGAAGTGCACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 123
Db 561 CTGATGAAGTGCACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 620

QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
Db 621 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 657

RESULT 7
LOCUS AX019384 1362 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent W09940188.
ACCESSION AX019384
VERSION AX019384.1 GI:10043354
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1362)
AUTHORS Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
TITLE Tumor-associated antigen derivatives from the mage family, and
nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
Patent: W 9940188-A 10 12-AUG-1999;
JOURNAL SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)

FEATURES
source Location/Qualifiers
1..1362
/organism="Homo sapiens"
/db_xref="taxon:9606"

Medicine, Immunology; Asahi 67, Kurume, Fukuoka 830, Japan
(Tel:0942-31-7551, Fax:0942-31-7699)
2 (bases 1 to 1019)
Imai,Y., Shichijo,S., Yamada,A., Katayama,T., Yano,H. and Itoh,K.
Sequence analysis of the MAGE gene family encoding human
tumor-rejection antigens
Gene 160 (2), 287-290 (1995)
95369706
Location/Qualifiers
1..1019
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="M73"
66..1010
/standard_name="melanoma antigen-6"
/note="Nomenclature of MAGE-6 was according to MAGE gene's
27 nucleotide sequences of HLA-A1 binding motif (Traversari
etc., 1992)"
/codon_start=1
/evidence=experimental
/product="MAGE-6 protein"
/protein_id="BAA06842.1"
/db_xref="GI:1125016"
/translation="MPEERSQHCKPEEGLEARGEALGLVGAQAPATEBOEAASSST
LVEVTIGVPAAESPPQSGASLPTTMTPLWSQSYEDSSNQEESGPTFPDLE
SEFOAALSRRKAKLVHLLKYRAREPVTKAEMLSGVGNWQYFFVIFSKAGDSLOL
VFGIELMEVDPIGHVYIFATLGLSDGLGDNQIMPKTGFLIIILAIKAEGDCAPE
EKIWEELSVLEVFEGREDSIFGDPKLLTQYFVOENLYEVQVPGSDPACYEFLWGP
ALLETSYKVLHHMKISGGPRISYPLLHEWALREGEE"

BASE COUNT 224 a 284 c 292 g 219 t
ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 1019;
Best Local Similarity 100.0%; Pred. No. 6.3e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTCTGATCTTCAGCAAGCTTCGGTGCATCTTCCTTCGAGCTGGTCTTTGGCATCGAG 63
Db 501 TTCTTTCTCTGATCTTCAGCAAGCTTCGGTGCATCTTCCTTCGAGCTGGTCTTTGGCATCGAG 560

QY 64 CTGATGAAGTGCACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 123
Db 561 CTGATGAAGTGCACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 620

QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
Db 621 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 657

RESULT 7
LOCUS AX019384 1362 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent W09940188.
ACCESSION AX019384
VERSION AX019384.1 GI:10043354
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1362)
AUTHORS Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
TITLE Tumor-associated antigen derivatives from the mage family, and
nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
Patent: W 9940188-A 10 12-AUG-1999;
JOURNAL SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)

FEATURES
source Location/Qualifiers
1..1362
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 345 a 348 c 383 g 286 t
ORIGIN /note="Melanoma tissue"

Query Match 69.8%; Score 157; DB 6; Length 1362;
Best Local Similarity 100.0%; Pred. No. 6.3e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGATCTTCAGCAAGCTTCGATTCCCTTCGAGCTGGTCTTTGGCATCGAG 63
|||||
DB 826 TTCTTTCTGATCTTCAGCAAGCTTCGATTCCCTTCGAGCTGGTCTTTGGCATCGAG 865
|||||
QY 64 CTGATGAAGTGAGCCCATCGGCGACGTGTACATCTTTGCCACCTCGCTGGCCTCTCC 123
|||||
DB 886 CTGATGAAGTGAGCCCATCGGCGACGTGTACATCTTTGCCACCTCGCTGGCCTCTCC 945
|||||
QY 124 TACATGGCCTGCTGGGTGACATCATGATGCCCA 160
|||||
DB 946 TACATGGCCTGCTGGGTGACATCATGATGCCCA 982
|||||

RESULT 8

HSU10691 HSI10691 3871 bp DNA linear PRI 23-JUN-1995
LOCUS Human MAGE-6 antigen (MAGE6) gene, complete cds.
DEFINITION
ACCESSION U10691
VERSION U10691.1 GI:533522
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3871)
AUTHORS De Plaen, E., Arden, K., Traversari, C., Gaforio, J. J., Szikora, J. P.,
De Smet, C., Brasseur, F., van der Bruggen, P., Lethe, B.,
Lurquin, C., Brasseur, R., Chomez, P., De Backer, O., Cavenee, W. and
Boon, T.
TITLE Structure, chromosomal localization, and expression of 12 genes of
the MAGE family
JOURNAL Immunogenetics 40 (5), 360-369 (1994)
MEDLINE 95012457
REFERENCE 2 (bases 1 to 3871)
AUTHORS De Plaen, E.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for
Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium
FEATURES
source
1. .3871
/organism="Homo sapiens"
/isolate="patient M2"
/db_xref="taxon:9606"
/chromosome="X"
/sex="female"
/cell_type="lymphocyte"
/tissue_type="blood"
/dev_stage="adult"
2053. .2118
/number=2
2199. .>3762
/number=3
2264. .3208
/gene="MAGE6"
2264. .3208
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/codon_start=1
/product="MAGE-6 antigen"
/protein_id="AA68875.1"
/db_xref="GI:533523"
/translation="MPLEQRSHCKPEGLRGEALGLVGAQAPATEEQEAASSTT
LVEVTGLVEPAESPPDPOGASLPTTMYPLWNSQVSDSSNOEGPSTFPDLE
SEQAALSRVAKLVHLLKYPAREVPTKAMGLSVGVNWOYFFPVFISKDSLQ
VFGLMEVDPIGHVYIFATCLGLSLDGLLDNQIMPKTGFLIIILAIKESGDAPE

EKINBELSVLEVFEGREDSIFGDPKLLTOYFQBNLYLEVRQVPGSDPACYEFLMGPR
ALIETSYKVLHMHMKISGGPRISPLLHHEWALREGEE"
BASE COUNT 865 a 1050 c 1117 g 839 t
ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 3871;
Best Local Similarity 100.0%; Pred. No. 6.6e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGATCTTCAGCAAGCTTCGATTCCCTTCGAGCTGGTCTTTGGCATCGAG 63
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DB 2699 TTCTTTCTGATCTTCAGCAAGCTTCGATTCCCTTCGAGCTGGTCTTTGGCATCGAG 2758
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QY 64 CTGATGAAGTGAGCCCATCGGCGACGTGTACATCTTTGCCACCTCGCTGGCCTCTCC 123
|||||
DB 2759 CTGATGAAGTGAGCCCATCGGCGACGTGTACATCTTTGCCACCTCGCTGGCCTCTCC 2818
|||||
QY 124 TACATGGCCTGCTGGGTGACATCATGATGCCCA 160
|||||
DB 2819 TACATGGCCTGCTGGGTGACATCATGATGCCCA 2855
|||||

RESULT 9

AF002997 AF002997 245077 bp DNA linear PRI 13-APR-2001
LOCUS Homo sapiens chromosome X map Xq28, complete sequence.
DEFINITION
ACCESSION AF002997
VERSION AF002997.2 GI:13621226
KEYWORDS HTG; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 9444 to 72299)
AUTHORS Gloeckner, G., Rosenthal, A., Drescher, B., Schattevoy, R., Poustka, A. and
Kioschis, P.
TITLE Genomic sequence in Xq28
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 245077)
AUTHORS Galocz, P., Schilhabel, M., Rosenthal, A. and Platzner, M.
TITLE Chromosome X genomic sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 245077)
AUTHORS Gloeckner, G., Rosenthal, A., Drescher, B. and Schattevoy, R.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE 4 (bases 1 to 245077)
AUTHORS Platzner, M.
TITLE Direct Submission
JOURNAL Submitted (13-APR-2001) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT On Apr 13, 2001 this sequence version replaced gi:4409798.
FEATURES
source
1. .245077
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xq28"
1. .211945
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP1-14D6"
/clone_lib="RPCI human PAC library 1"
9444. .45606
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LM0411, cosmid"
20074. .226999
/organism="Homo sapiens"
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70149 a 53336 c 52595 g 68996 t 1 others
BASE COUNT 70149 a 53336 c 52595 g 68996 t 1 others
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Query Match 69.8%; Score 157; DB 9; Length 245077;
Best Local Similarity 100.0%; Pred. No. 7.6e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGGCAGCTGGTCTTTGGCATCGAG 63
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Db 164123 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGGCAGCTGGTCTTTGGCATCGAG 164182
|||||

QY 64 CTGATGAAGTGAGCCCGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 123
|||||
Db 164183 CTGATGAAGTGAGCCCGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 164242
|||||

QY 124 TACGATGGCTGCTGGGTGACATCAGATCATGCCCA 160
|||||
Db 164243 TACGATGGCTGCTGGGTGACATCAGATCATGCCCA 164279
|||||

RESULT 10
AX019380
LOCUS AX019380 1212 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent WO9940188.
ACCESSION AX019380
VERSION AX019380.1 GI:10043352
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1212)
AUTHORS Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
TITLE Tumor-associated antigen derivatives from the mage family, and
nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
JOURNAL Patent: WO 9940188-A 6 12-AUG-1999;
SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES
source
location/Qualifiers
1..1212
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Melanoma tissue"
BASE COUNT 289 a 319 c 344 g 260 t
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Best Local Similarity 99.2%; Pred. No. 4.1e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTTTGGCATCGAGCTGATGAAGTGCACCCATCGCCACGTGTA 95
|||||
Db 708 TTCCTTGCAGCTGCTTTGGCATCGAGCTGATGAAGTGCACCCATCGCCACGTGTA 767
|||||

QY 96 CATCTTTGCCACCTGCCCTGCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 768 CATCTTTGCCACCTGCCCTGCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 827
|||||

QY 156 GCCCA 160
|||||

Query Match 32.9%; Score 74; DB 6; Length 1353;
Best Local Similarity 99.2%; Pred. No. 4.1e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 849 TTCCTTGCAGCTGCTTTGGCATCGAGCTGATGAAGTGCACCCATCGCCACGTGTA 908
|||||

QY 96 CATCTTTGCCACCTGCCCTGCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 909 CATCTTTGCCACCTGCCCTGCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 968
|||||

QY 156 GCCCA 160
|||||
Db 969 GCCCA 973
|||||

RESULT 12
AX343855
LOCUS AX343855 1569 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 1 from Patent WO0200892.
ACCESSION AX343855
VERSION AX343855.1 GI:18491925
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (sites)
AUTHORS cabezon Silva,T.E. and Delisse,A.M.
TITLE Triple fusion proteins comprising ubiquitin fused between
thioredoxin and a polypeptide of interest
JOURNAL Patent: WO 0200892-A 1 03-JAN-2002;
SmithKline Beecham Biologics SA (BE)
FEATURES
source
location/Qualifiers
1..1569
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Chimaeric (E. coli - human)"
BASE COUNT 391 a 400 c 433 g 345 t
ORIGIN
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Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||
QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 1125 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 1184
|||||
QY 156 GCCCA 160
|||||
Db 1185 GCCCA 1189

RESULT 13
LOCUS AR153502 1640 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6235525.
ACCESSION AR153502
VERSION AR153502.1 GI:15121034
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1640)
AUTHORS van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.
TITLE Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof
JOURNAL Patent: US 6235525-A 11 22-MAY-2001;
FEATURES
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BASE COUNT 380 a 402 c 457 g 401 t
ORIGIN

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Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
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|||||
QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 699 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 758
|||||
QY 156 GCCCA 160
|||||
Db 759 GCCCA 763

RESULT 14
LOCUS I36926 1640 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 11 from patent US 5612201.
ACCESSION I36926
VERSION I36926.1 GI:2084886
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1640)
AUTHORS De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C. and Chomez,P.
TITLE Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor
JOURNAL Patent: US 5612201-A 11 18-MAR-1997;
FEATURES
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    source
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source
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Query Match      32.9%; Score 74; DB 6; Length 1640;
Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
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Db 639 TTCCTTGCAGCTGCTTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 698
|||||
QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 699 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 758
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QY 156 GCCCA 160
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Db 759 GCCCA 763

RESULT 15
LOCUS BC011744 1663 bp mRNA linear PRI 02-AUG-2001
DEFINITION Homo sapiens, Similar to melanoma antigen, family A, 3, clone MGC:19667 IMAGE:3345801, mRNA, complete cds.
ACCESSION BC011744
VERSION BC011744.1 GI:15079897
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1663)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcgaps-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DMP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgrl.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tlionson,E.E., Touchman,J.W., Tsugeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAL Plate: 27 Row: b Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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    /organism="Homo sapiens"
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    /tissue_type="Skin, melanotic melanoma."

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VFGIELMEVDPIGHLVIFATCIGLSYDGLGDNQIMPKAGLLIIVLAIAREGDCAPE
EKIWEELSVLEVEFGREDSILGDPKKLLTQHVFQENYLEYRQVPGSDPACYEFLWGPR
ALVETSYVKVYLHHMVKISGGPHISYPPLHEWVLRGEE"
BASE COUNT      411 a      398 c      448 g      406 t
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Query Match      32.9%; Score 74; DB 9; Length 1663;
Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  36  TTCCTTCAGCTGCTCTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 95
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Db  612 TTCCTTCAGCTGCTCTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 671
    |||||||||||||||||||||||||||||||||||||||||||||||||||

QY  96  CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCCTGCTGGGTGACATCAGATCAT 155
    |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  672 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCCTGCTGGGTGACATCAGATCAT 731
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QY  156 GCCCA 160
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Db  732 GCCCA 736
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2002, 22:39:08 ; Search time 257.01 Seconds
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Title: US-08-037-230D-18

Perfect score: 225

Sequence: 1 TATTTCCTTCCTGATCTT.....CGGACTGTCCTGAGGAG 225

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : N_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	225	100.0	225	13	AA032362
2	225	100.0	225	15	AA072487
3	225	100.0	225	20	AA084122
4	174	77.3	225	16	AA0701166
5	157	69.8	1362	20	AA087596
6	157	69.8	1375	19	AA072716
7	157	69.8	4204	22	AA02056
8	74	32.9	666	22	AA018141
9	74	32.9	945	22	AA012993

10	74	32.9	1212	20	AA087592
11	74	32.9	1353	20	AA087588
12	74	32.9	1640	15	AA072480
13	74	32.9	1640	20	AA084116
14	74	32.9	4204	20	AA026974
15	74	32.9	4204	21	AA037927
16	74	32.9	4204	22	AA018140
17	69	30.7	379	18	AA063345
18	69	30.7	1640	13	AA032355
19	56	24.9	268	18	AA063347
20	56	24.9	376	18	AA063346
21	49	21.8	271	18	AA063350
22	49	21.8	378	18	AA063349
23	43	19.1	271	18	AA063348
24	36	16.0	727	22	AA021285
25	36	16.0	920	22	ABA36364
26	36	16.0	920	22	AA024300
27	36	16.0	920	22	AA049576
28	36	16.0	1956	22	ABA26487
29	36	16.0	1956	22	AA015118
30	36	16.0	1956	22	AA036453
31	36	16.0	4157	13	AA032353
32	36	16.0	4157	15	AA072478
33	36	16.0	4157	20	AA084114
34	27	12.0	27	15	AA044759
35	27	12.0	27	17	AA035415
36	26	11.6	26	20	AA028066
37	26	11.6	1030	22	AA021286
38	26	11.6	4523	22	AA006131
39	24	10.7	24	16	AA050085
40	24	10.7	24	21	AA035541
41	24	10.7	24	22	AA084241
42	24	10.7	24	22	AA067098
43	24	10.7	27	24	ABA01874
44	24	10.7	44	18	AA060633
45	23	10.2	31	21	AA09232

ALIGNMENTS

RESULT 1

AA032362
ID AA032362 standard; DNA; 225 BP.

XX AC AA032362;

XX DF 22-APR-1993 (first entry)

XX DE MAGE-6 gene.

XX KW Melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.

XX OS Homo sapiens.

XX PN WO9220356-A.

XX PD 26-NOV-1992.

XX PF 22-MAY-1992; 92WO-US04354.

XX PR 23-MAY-1991; 91US-0705702.

XX PR 09-JUL-1991; 91US-0728838.

XX PR 23-SEP-1991; 91US-0764364.

XX PR 12-DEC-1991; 91US-0807043.

XX (LUDW-) LUDWIG INST CANCER RES.

XX PI Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;

XX PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;

XX DR WPI; 1992-415460/50.

XX Nucleic acid mol. encoding a human tumour rejection antigen
 PT precursor - useful as an immunostimulant in a vaccine for
 PT treating and preventing cancers, also useful in diagnosis
 XX
 PS Disclosure; Page 88; 142pp; English.
 XX
 CC The sequences given in AAQ32352-69 represent a new family of genes
 CC referred to as melanoma antigens (MAGE). The cDNAs of this gene
 CC family were identified during the isolation of the antigen E gene.
 CC The MAGE cDNAs, when tested, did not transfer expression of antigen
 CC E, but they did show substantial homology to the antigen E cDNA
 CC sequence. The MAGE DNAs share a certain degree of homology with each
 CC other and are expressed in tumour cells including several types of
 CC human tumor cells as well as in human tumors. MAGE expression is not
 CC restricted to melanomas. MAGE refers to a family of tumor rejection
 CC antigen precursors. The antigens resulting from these genes are
 CC referred to as MAGE TRAS or melanoma antigen tumor rejection antigens.
 CC See also AAQ32351.
 XX
 SQ Sequence, 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 13; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.1e-105;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCGAGCTGCTTTGGCATC 60
 DB 1 tattttctctgtgatcttcagcaagcttcgattcccttgagctggtctttggcatc 60
 QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGCCACCTGCCTGGGCTC 120
 DB 1 tattttctctgtgatcttcagcaagcttcgattcccttgagctggtctttggcatc 60
 QY 61 gagctgatggaagtggaccccatcgccaogtgtacatctttggcactgctgggctc 120
 DB 61 gagctgatggaagtggaccccatcgccaogtgtacatctttggcactgctgggctc 120
 QY 121 TCCTACGATGCTGCTGGTGGTGAACAATCAGATCATGCCAGGACAGCTTCTCTGATAATC 180
 DB 121 tcttaccatggtcctgcggtgggagcaatcagatcatgccagagcaggtcttctgataatc 180
 QY 181 ATCTTGCCCATATTCGCAAGAGGGGAGCTGTGCCCTGAGGAG 225
 DB 181 atcttgcccataatcgcaagagggcgactgtgccccctgaggag 225

RESULT 2
 AAQ72487
 ID AAQ72487 standard; cDNA to mRNA; 225 BP.
 XX
 AC AAQ72487;
 XX
 DT 22-JUN-1995 (first entry)
 XX
 DE Tumour rejection antigen MAGE-6 cDNA.
 XX
 KW Tumour rejection antigen; melanoma antigen-6; MAGE-6; MAGE-3;
 KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN W09423031-A.
 XX
 PD 13-OCT-1994.
 XX
 PF 17-MAR-1994; 94WO-US02877.
 XX
 PR 26-MAR-1993; 93US-0037230.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Boon-falleur T, Gaugler B, Van Den EYNDE B, Van DER BRUGGEN P;
 XX WPT; 1994-333192/41.
 DR

XX New tumour rejection antigen precursor MAGE3 - useful in
 PT treatment and diagnosis of cancer
 XX
 PS Example 32; Page 73; 105pp; English.
 XX
 CC AAQ72487 is the cDNA sequence which codes for melanoma antigen-6
 CC (MAGE-6). Another melanoma antigen MAGE-3 is encoded by
 CC AAQ72470, this is a tumour rejection antigen precursor. Melanomas
 CC characterised by the expression of MAGE-3 can be detected, or
 CC monitored, by contacting a test sample with an agent that can
 CC recognise MAGE-3. The melanoma can be treated by the administration
 CC of cytolytic T cells specific for the complex of antigen D (the
 CC mature rejection antigen derived from MAGE-3) and a human leucocyte
 CC antigen (esp. HLA-A1).
 XX
 SQ Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 15; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.1e-105;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCGAGCTGCTTTGGCATC 60
 DB 1 tattttctctgtgatcttcagcaagcttcgattcccttgagctggtctttggcatc 60
 QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGCCACCTGCCTGGGCTC 120
 DB 61 gagctgatggaagtggaccccatcgccaogtgtacatctttggcactgctgggctc 120
 QY 121 TCCTACGATGCTGCTGGTGGTGAACAATCAGATCATGCCAGGACAGCTTCTCTGATAATC 180
 DB 121 tcttaccatggtcctgcggtgggagcaatcagatcatgccagagcaggtcttctgataatc 180
 QY 181 ATCTTGCCCATATTCGCAAGAGGGGAGCTGTGCCCTGAGGAG 225
 DB 181 atcttgcccataatcgcaagagggcgactgtgccccctgaggag 225

RESULT 3
 AAX84122
 ID AAX84122 standard; cDNA; 225 BP.
 XX
 AC AAX84122;
 XX
 DT 08-SEP-1999 (first entry)
 XX
 DE MAGE-6 gene.
 XX
 KW Tumour rejection antigen; vaccine; cancer; MAGE-6 gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US5925729-A.
 XX
 PD 20-JUL-1999.
 XX
 PF 02-MAY-1994; 94US-0142368.
 XX
 PR 02-MAY-1994; 94US-0142368.
 PR 23-MAY-1991; 91US-0705702.
 PR 09-JUL-1991; 91US-0728838.
 PR 23-SEP-1991; 91US-0764365.
 PR 12-DEC-1991; 91US-0807043.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
 PI Van Den EYNDE B, Van Der Bruggen P, Van Pel A;
 XX WPT; 1999-418294/35.
 DR
 XX

PT New tumour rejection antigen is useful as a vaccine against
PT cancerous diseases
XX
XX
PS Disclosure; Column 69-70; 58pp; English.
XX
CC This sequence represents the MAGE-6 gene sequence.
CC The invention relates to a tumour rejection antigen sequence that is
CC useful as a tumour rejection antigen for vaccination against cancerous
CC conditions.
XX
SQ Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1e-105;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGAGTTCCTTGCAGCTGGTCTTTGGCCTC 60
Db 1 tattttcttctgtatcttcagcaagcttcagattcttgcagctggtctttggcctc 60
Qy 61 GAGCTGATGGAAGTGGACCCCATCGCCACCTGTACATCTTTGCCACCTGCTGGCCTC 120
Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccacctgctggcctc 120
Qy 121 TCCTACGATGCGCTGGTGGTGACAATCAGATCATGCCCCAGGACAGGCTTCTCTGATAATC 180
Db 121 tcttacctgagtcctgctgggtgacaatcagatcatgccccagagcaggtcttctgataatc 180
Qy 181 ATCTTGCCCATTAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
Db 181 atcttgcccaataatcgcaagaggcgactgtgccccctgaggag 225

RESULT 4
AAAT01166
ID AAAT01166 standard; DNA; 225 BP.
XX
AC AAAT01166;
XX
DT 26-FEB-1996 (first entry)
XX
DE MAGE-6 gene.
XX
KW MAGE-6; melanoma; tumour rejection antigen; cancer; diagnosis; ss.
XX
OS Homo sapiens.
XX
FN WO9523874-A1.
XX
PD 08-SEP-1995.
XX
PF 23-FEB-1995; 95WO-US02203.
XX
PR 30-NOV-1994; 94US-0346774.
PR 01-MAR-1994; 94US-0204727.
PR 10-MAR-1994; 94US-0209172.
PR 01-SEP-1994; 94US-0299849.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
PI De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
XX
DR WPI; 1995-320586/41.
XX
PT Determn. of cancerous condition(s) - using a nucleic acid as a
PT primer to determine expression of a MAGE tumour rejection antigen
PT precursor
XX
PS Example 32; Page 80; 121pp; English.
XX

CC A family of human tumour rejection antigen precursor, MAGE, genes
CC (AAAT0091-99, AAAT0165-71) was isolated from various tumour cell lines.
CC cDNA (AAAT01166) coding for MAGE-6 was obtd. from human melanoma
CC LB-33-MEL cells. MAGE serve as markers for tumour diagnosis. The
CC genes are silent in normal cells.
XX
SQ Sequence 225 BP; 44 A; 66 C; 57 G; 58 T; 0 other;
Query Match 77.3%; Score 174; DB 16; Length 225;
Best Local Similarity 99.6%; Pred. No. 3.6e-79;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGAGTTCCTTGCAGCTGGTCTTTGGCCTC 60
Db 1 tattttcttctgtatcttcagcaagcttcagattcttgcagctggtctttggcctc 60
Qy 61 GAGCTGATGGAAGTGGACCCCATCGCCACCTGTACATCTTTGCCACCTGCTGGCCTC 120
Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccacctgctggcctc 120
Qy 121 TCCTACGATGCGCTGGTGGTGACAATCAGATCATGCCCCAGGACAGGCTTCTCTGATAATC 180
Db 121 tcttacctgagtcctgctgggtgacaatcagatcatccccagagcaggtcttctgataatc 180
Qy 181 ATCTTGCCCATTAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
Db 181 atcttgcccaataatcgcaagaggcgactgtgccccctgaggag 225
RESULT 5
AAAX87596
ID AAAX87596 standard; cDNA; 1362 BP.
XX
AC AAAX87596;
XX
DT 26-OCT-1999 (first entry)
XX
DE CLYTA-MAGE-3-His fusion DNA.
XX
KW MAGE-3; CLYTA-MAGE-3-His; fusion protein; tumour; melanoma;
KW breast cancer; bladder cancer; lung cancer; colon cancer;
KW head and squamous cell carcinoma; oesophagus carcinoma; vaccine;
KW human; ss.
XX
OS Chimeric - Streptococcus pneumoniae.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
FN WO9940188-A2.
XX
PD 12-AUG-1999.
XX
PF 02-FEB-1999; 99WO-EP00660.
XX
PR 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX
DR WPI; 1999-494293/41.
DR P-PSDB; AAY06593.
XX
PT New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast
XX
PS Example 10; Page 72; 72pp; English.
XX
CC This DNA sequence codes for a fusion protein (see AAY06593) composed
CC of the C-terminal portion of the Streptococcus pneumoniae LYTA

CC protein (CLYTA), the human MAGE-3 tumour-associated antigen and a
 CC hexahistidine tail. A vector designed for recombinant expression
 CC of the fusion protein in Escherichia coli is provided. The CLYTA
 CC moiety provides expression of soluble fusion protein, facilitates
 CC affinity purification of the fusion protein, and also acts as a
 CC T-helper epitope. The invention relates to MAGE proteins fused to
 CC an immunological fusion partner, e.g. CLYTA-MAGE-3-His. These novel
 CC fusion proteins provide vaccines for immunotherapy of melanomas or
 CC other MAGE-associated tumours like breast, bladder, lung and
 CC non-small cell lung cancer, head and squamous cell carcinoma, colon
 CC carcinoma and oesophagus carcinoma.
 XX
 SQ Sequence 1362 BP; 345 A; 348 C; 383 G; 286 T; 0 other;

Query Match 69.8%; Score 157; DB 20; Length 1362;
 Best Local Similarity 100.0%; Pred. No. 1.8e-70;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCCTTGGCAGTGGTCTTTGGCATCGAG 63
 DB 826 ttcttctctgtatcttcagcaagcttcgagttccttgcagctggtctttggcatcgag 885
 QY 64 CTGATGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACTGCCTGGGCTCTCC 123
 DB 886 ctgatggaagtggaccccatcgccacgtgtacatctttgcccactgcctgggctctcc 945
 QY 124 TACGATGCCCTGCTGGGTGACAAATCAGATCATGCCCA 160
 DB 946 taccatggcctgctgggtgacaatcagatcatgccca 982

RESULT 6
 AAV22716
 ID AAV22716 standard; DNA; 1375 BP.
 XX
 AC AAV22716;
 XX
 DT 18-AUG-1998 (first entry)
 XX
 DE MAGE-6 cDNA.
 XX
 KW Human tumor rejection antigen precursor; TRA; MAGE-6; HLA-Cw*16;
 KW major histocompatibility complex; MHC; cytotoxic T-cell; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9810780-A1.
 XX
 PD 19-MAR-1998.
 XX
 PF 27-AUG-1997; 97WO-US15069.
 XX
 PR 13-SEP-1996; 96US-0713354.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Bocr-Falleur T, Deplaen E, Van Der Bruggen P;
 PI WPI; 1998-207144/18.
 XX
 DR Tumour rejection antigen precursor, MAGE-6 derived peptide(s) which
 DR bind to HLA-Cw*16 - used for provoking proliferation of cytotoxic T
 PT cells, useful for, e.g. treatment of cancerous cells
 PT
 PS Disclosure; Page 19; 31pp; English.
 XX

CC The present sequence represents a MAGE-6 cDNA encoding a human tumor
 CC rejection antigen (TRA) precursor. The invention provides for TRAs
 CC (AAW56268-W56272) which are processed from TRA precursors that are
 CC derived from the MAGE-6 gene. The TRAs bind to major histocompatibility
 CC complex (MHC) molecules of the type HLA-Cw*16 to provoke a cytotoxic
 CC T-cell response against cells exhibiting this particular TRA-MHC

CC complex. As the cells presenting these complexes are human cancerous
 CC cells, the TRA peptides are claimed to be useful in provoking lysis of
 CC these cancerous cells thereby providing a probable method of treating
 CC cancer.
 XX
 SQ Sequence 1375 BP; 293 A; 364 C; 404 G; 314 T; 0 other;

Query Match 69.8%; Score 157; DB 19; Length 1375;
 Best Local Similarity 100.0%; Pred. No. 1.8e-70;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCCTTGGCAGTGGTCTTTGGCATCGAG 63
 DB 595 ttcttctctgtatcttcagcaagcttcgagttccttgcagctggtctttggcatcgag 654
 QY 64 CTGATGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACTGCCTGGGCTCTCC 123
 DB 655 ctgatggaagtggaccccatcgccacgtgtacatctttgcccactgcctgggctctcc 714
 QY 124 TACGATGCCCTGCTGGGTGACAAATCAGATCATGCCCA 160
 DB 715 tacyatggcctgctgggtgacaatcagatcatgccca 751

RESULT 7
 AAS02056
 ID AAS02056 standard; CDNA; 4204 BP.
 XX
 AC AAS02056;
 XX
 DT 16-JUL-2001 (first entry)
 XX
 DE DNA encoding molecule for disease detection and treatment, mddt21.
 XX
 KW Human; mddt21; gene therapy; adenosine deaminase deficiency;
 KW ADA; severe combined immunodeficiency syndrome; cystic fibrosis;
 KW thalassaemia; familial hypercholesterolaemia; haemophilia; factor VIII;
 KW factor IX; cancer; cell proliferation; parasite; human retrovirus; HIV;
 KW hepatitis B; hepatitis C; Candida albicans; Plasmodium falciparum;
 KW Paracoccidioides brasiliensis; Trypanosoma brasiliensis; ss.

XX Homo sapiens.
 OS
 PN WO200123538-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000WO-US26085.
 XX
 PR 28-SEP-1999; 99US-0156565.
 PR 30-NOV-1999; 99US-0168197.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
 PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
 PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR;
 PI Roseberry AM, Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK;
 PI Anshey S, Fong WT,
 XX WPI; 2001-258131/26.
 XX
 DR Purified disease treatment and detection molecule polynucleotides and
 DR polypeptides, useful for providing diagnostic assays and gene therapy -
 PT
 PS Claim 1; Page 109-110; 113pp; English.

CC The sequence represents the coding sequence of molecule for disease
 CC detection and treatment, mddt21, shown by computer analysis to be similar
 CC to the MAGE family of proteins. The sequence may be used for
 CC somatic or germline gene therapy. Gene therapy may be performed to: (i)
 CC correct genetic deficiency such as in severe combined immunodeficiency

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CC syndrome associated with adenosine deaminase (ADA) deficiency, cystic
CC fibrosis, thalassaemias, familial hypercholesterolaemia and haemophilia
CC caused by factor VIII or factor IX deficiencies; (ii) express a
CC conditional lethal gene product (such as in the case of cancers which
CC result from unregulated cell proliferation); (iii) express a protein
CC which affords protection against intracellular parasites (for example,
CC human retroviruses such as HIV, hepatitis B or C, fungal parasites such
CC as Candida albicans and Paracoccidioides brasiliensis, and protozoal
CC parasites such as Plasmodium falciparum and Trypanosoma brasiliensis.
XX
SQ Sequence 4204 BP; 947 A; 1145 C; 1219 G; 893 T; 0 other;

Query Match          69.8%; Score 157; DB 22; Length 4204;
Best Local Similarity 100.0%; Pred. No. 1.9e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTGGCATCGAG 63
Db 2900 ttcttctgtgatcttcagcaagcttcgagattcccttgagctggtctttggcatcgag 2959

QY 64 CTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123
Db 2960 ctgatggaagtggaccccatcggccacgtgtacatctttgccacctgcctgggacctcc 3019

QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCCA 160
Db 3020 tacgatggcctgctgggtgacaaatcagatcatgcccc 3056

RESULT 8
AAD18141
ID AAD18141 standard; cDNA; 666 BP.
XX
AC AAD18141;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human melanoma associated antigen 3 (MAGE-3) truncated cDNA.
XX
KW Human; melanoma associated antigen 3; MAGE-3; neuroprotective; neurotropic;
KW immunosuppressive; caspase-12 activation; cell death related disease;
KW cell death inhibitor; cancer-specific protein; Alzheimer's disease;
KW neurodegenerative disease; autoimmune disease; amyotrophy; gene therapy;
KW organ disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..666
FT /*tag= a
FT /product= "Human MAGE-3 protein"
FT /note= "CDS does not include start codon"
FT /partial
XX
PN EP1126027-A1.
XX
PD 22-AUG-2001.
XX
PF 16-FEB-2001; 2001EP-0301361.
XX
PR 18-FEB-2000; 2000JP-0041927.
XX
PA (RIKE ) RIKEN KK.
XX
PI Morishima N, Shibata T;
XX
DR WPI; 2001-591501/67.
DR P-PSDB; AAE10673.
XX
PT New polypeptide for treating cell death related diseases such as
PT Alzheimer's disease, neurodegenerative diseases, autoimmune diseases,
PT amyotrophy and organ disorders comprises the recombinant
```

```
PT cancer-specific protein MAGE-3 -
XX
PS Claim 3; Page 25-27; 41pp; English.
XX
CC The present sequence is the truncated form of human melanoma
CC associated antigen 3 (MAGE-3) cDNA. The present invention relates
CC to MAGE-3 protein or its truncated form which specifically bind to
CC caspase-12 or pro-caspase-12 protein and inhibit their activation.
CC MAGE-3 proteins are cancer-specific proteins and are used as cell-
CC death inhibitors. Therapeutic agents comprising MAGE-3 sequence are
CC useful for treating cell death related diseases such as Alzheimer's
CC disease, neurodegenerative diseases, autoimmune diseases, amyotrophy
CC and organ disorders. MAGE-3 gene is useful as an agent for gene therapy.
CC The sequences of the invention are useful for preventing or treating a
CC cell death-related disease developing in tissues in the nervous system,
CC vascular system, respiratory system, digestive system, lymph system,
CC urinary system, or reproductive system.
XX
SQ Sequence 666 BP; 151 A; 165 C; 197 G; 153 T; 0 other;

Query Match          32.9%; Score 74; DB 22; Length 666;
Best Local Similarity 99.2%; Pred. No. 4.8e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCGAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCGCATGTA 95
Db 189 ttcttgcagctggtctttggcatcgagctgatggaagtggaccccatcgccacttgta 248

QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCCCTGTGGTGACAAATCAGATCAT 155
Db 249 catctttgccacctgcctgggccctctctacgatggcctgtgggtgacaatcagatcat 308

QY 156 GCCCA 160
Db 309 gccca 313

RESULT 9
AAD12993
ID AAD12993 standard; DNA; 945 BP.
XX
AC AAD12993;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human MAGE-A3 DNA.
XX
KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;
KW gene therapy; human; MAGE-A3; tumour rejection antigen; TRA; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..945
FT /*tag= a
FT /product= "MAGE-A3 protein"
XX
PN WO200153833-A1.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US02008.
XX
PR 20-JAN-2000; 2000US-0177242.
PR 25-OCT-2000; 2000US-0243212.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;
```

PI Demotte N, Schultz E;
 XX WPI; 2001-488724/53.
 DR P-PSDB; AAE06853.
 XX
 XX Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
 PT HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
 PT in diagnosis and treatment of a disorder characterized by expression of
 PT MAGE-A1 or -A3 -
 XX
 XX Example 3; Page 94-95; 103pp; English.
 XX
 XX The invention relates to functional variants and isolated mimetics of a
 CC MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
 CC or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described
 CC in the specification. MAGE genes encode tumour rejection antigens
 CC (TRAS) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.
 CC The MAGE antigenic peptide acts by binding to HLA molecules
 CC on tumour cells and stimulating recognition of these cells and thus
 CC signalling them to the immune system for destruction. The peptide when
 CC presented by HLA molecule induces the activation and stimulation of
 CC CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to
 CC treat and diagnose disorders characterised by expression of MAGE-A1
 CC or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,
 CC head and neck, breast, colorectal, prostate, renal, bladder,
 CC hepatocellular, papillary thyroid and gastric carcinomas, myelomas,
 CC brain tumours, sarcomas, seminomas, and ovarian tumours. The present
 CC sequence is human MAGE-A3 DNA.
 XX
 SQ Sequence 945 BP; 210 A; 254 C; 278 G; 203 T; 0 other;

Query Match 32.9%; Score 74; DB 22; Length 945;
 Best Local Similarity 99.2%; Pred. No. 4.9e-28;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 36 TTCCTTGAGCTGGTCTTTGGCATGCGAGCTGATGGAAGTGGACCCCATCGGCCACGTTGA 95
 Db 468 ttccttgagctggtctttggcatgctgagctgagtggaagtggaccccatcgccactgtga 527
 Qy 96 CATCTTTGCCACCTGCGCCCTCTCTCTAGCATGGCCCTGCTGGTGACATCAGATCAT 155
 Db 528 catctttgccacctgctggcctctctctacgatggcctgctggtgacacatcgatcat 587
 Qy 156 GCCCA 160
 Db 588 gccca 592

RESULT 10
 AAX87592
 ID AAX87592 standard; cDNA; 1212 BP.
 AC AAX87592;
 XX
 XX 26-OCT-1999 (first entry)
 DT
 XX
 DE Haemagglutinin-MAGE-3-His fusion DNA.
 XX
 KW MAGE-3; haemagglutinin; NSI-MAGE-3-His; fusion protein; tumour;
 KW melanoma; breast cancer; bladder cancer; lung cancer;
 KW head and squamous cell carcinoma; colon cancer;
 KW oesophagus carcinoma; vaccine; human; ss.
 XX
 OS Chimeric - Influenza virus.
 OS Chimeric - Homo sapiens.
 OS Chimeric - synthetic.
 XX
 PN WO9940188-A2.
 XX
 PD 12-AUG-1999.
 XX
 PF 02-FEB-1999; 99WO-EP00660.

XX
 PR 06-FEB-1998; 98GB-0002650.
 PR 05-FEB-1998; 98GB-0002543.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 XX Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
 PI
 XX WPI; 1999-494293/41.
 DR P-PSDB; AAY06591.
 XX
 XX New protein derivatives used in cancer vaccine therapy for treating
 PT a range of cancers including melanomas, carcinomas and cancers of
 PT breast
 PT
 XX Example 7; Page 69; 72pp; English.
 PS
 XX This DNA sequence codes for a fusion protein (see AAY06591) composed
 CC of haemagglutinin NSI of influenza virus, the human MAGE-3
 CC tumour-associated antigen and a hexahistidine tail. A vector
 CC designed for recombinant expression of the fusion protein is
 CC provided. MAGE-3 cDNA was amplified using primers that altered the
 CC first 5 codons to Escherichia coli codon usage. The NSI moiety
 CC provided the fusion protein with additional exogenous T-helper
 CC epitopes. The invention relates to MAGE proteins fused to an
 CC immunological fusion partner, e.g. NSI-MAGE-3-His. These novel
 CC fusion proteins provide vaccines for immunotherapy of melanomas or
 CC other MAGE-associated tumours like breast, bladder, lung and
 CC non-small cell lung cancer, head and squamous cell carcinoma, colon
 CC carcinoma and oesophagus carcinoma.
 XX
 SQ Sequence 1212 BP; 289 A; 319 C; 344 G; 260 T; 0 other;

Query Match 32.9%; Score 74; DB 20; Length 1212;
 Best Local Similarity 99.2%; Pred. No. 4.9e-28;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 36 TTCCTTGAGCTGGTCTTTGGCATGCGAGCTGATGGAAGTGGACCCCATCGGCCACGTTGA 95
 Db 708 ttccttgagctggtctttggcatgctgagctgagtggaagtggaccccatcgccactgtga 767
 Qy 96 CATCTTTGCCACCTGCGCCCTCTCTCTAGCATGGCCCTGCTGGTGACATCAGATCAT 155
 Db 768 catctttgccacctgctggcctctctctacgatggcctgctggtgacacatcgatcat 827
 Qy 156 GCCCA 160
 Db 828 gccca 832

RESULT 11
 AAX87588
 ID AAX87588 standard; cDNA; 1353 BP.
 AC AAX87588;
 XX
 XX 26-OCT-1999 (first entry)
 DT
 XX
 DE Lipoprotein D-MAGE-3-His fusion DNA.
 XX
 KW MAGE-3; lipoprotein D; LPD-MAGE-3-His; fusion protein; tumour;
 KW melanoma; breast cancer; bladder cancer; lung cancer;
 KW head and squamous cell carcinoma; colon cancer;
 KW oesophagus carcinoma; vaccine; human; ss.
 XX
 OS Chimeric - Haemophilus influenzae.
 OS Chimeric - Homo sapiens.
 OS Chimeric - synthetic.
 XX
 PN WO9940188-A2.
 XX
 PD 12-AUG-1999.

```
XX 02-FEB-1999; 99WO-EP00660.
XX 06-FEB-1998; 98GB-0002650.
XX 05-FEB-1998; 98GB-0002543.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX WPI; 1999-494293/41.
XX P-PSDB; AAY06589.
XX New protein derivatives used in cancer vaccine therapy for treating
XX a range of cancers including melanomas, carcinomas and cancers of
XX breast
XX Example 1; Page 66; 72pp; English.
XX This DNA sequence codes for a fusion protein (see AAY06589) composed
XX of lipidated protein D (LPD) of Haemophilus influenzae B, the human
XX MAGE-3 tumour-associated antigen and a hexahistidine tail. A
XX vector designed for recombinant expression of the fusion protein is
XX provided. MAGE-3 cDNA was amplified using primers that altered the
XX first 5 codons to Escherichia coli codon usage. The LPD moiety
XX provided the fusion protein with additional exogenous T-cell
XX epitopes and also increased expression levels in E. coli. The
XX lipid tail ensured optimal presentation of the antigen to
XX antigen-presenting cells. The affinity tag facilitated
XX purification. The invention relates to MAGE-3-His. These novel
XX immunological fusion partner, e.g. LPD-MAGE-3-His. These novel
XX fusion proteins provide vaccines for immunotherapy of melanomas or
XX other MAGE-associated tumours like breast, bladder, lung and
XX non-small cell lung cancer, head and squamous cell carcinoma, colon
XX carcinoma and oesophagus carcinoma.
XX Sequence 1353 BP; 342 A; 337 C; 354 G; 320 T; 0 other;

Query Match 32.9%; Score 74; DB 20; Length 1353;
Best Local Similarity 99.2%; Pred. No. 4.9e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95.
Db 849 ttctctgcagctggtctttggcatcgagctgagtggaagtggaacccatcgccactgtga 908

QY 96 CATCTTTGCCACCTGCTTGGCCCTCTCTAGCATGGCCTGCTGGTGACAAATCAGATCAT 155
Db 909 catctttgccacctgacctggccctctctactacgatggcctgctgggtgacaatcagatcat 968

QY 156 GCCCA 160
Db 969 gccca 973

RESULT 12
AAQ72480
ID AAQ72480 standard; cDNA to mRNA; 1640 BP.
XX
XX AAQ72480;
XX
XX 22-JUN-1995 (first entry)
XX Tumour rejection antigen precursor MAGE-3 cDNA.
XX Tumour antigen rejection precursor; melanoma antigen-3; MAGE-3;
XX cancer; cytolytic T cells; antigen D; human leucocyte antigen;
XX PIA gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
```

```
FT CDS 172..1116
FT FT /*tag= a
XX
XX WO9423031-A.
XX
XX 13-OCT-1994.
XX
XX 17-MAR-1994; 94WO-US02877.
XX
XX 26-MAR-1993; 93US-0037230.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
XX WPI; 1994-333192/41.
XX
XX New tumour rejection antigen precursor MAGE3 - useful in
XX treatment and diagnosis of cancer
XX Example 32; Page 64; 105pp; English.
XX AAQ72480 is the P1A gene fragment which contains the cDNA coding
XX sequence AAQ72470, which encodes melanoma antigen-3 (MAGE-3), a tumour
XX rejection antigen precursor. Melanomas characterised by the expression of
XX MAGE-3 can be detected, or monitored, by contacting a test sample with
XX an agent that can recognise MAGE-3. The melanoma can be treated by the
XX administration of cytolytic T cells specific for the complex of
XX antigen D (the mature rejection antigen derived from MAGE-3) and a
XX human leucocyte antigen (esp. HLA-A1).
XX Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;

Query Match 32.9%; Score 74; DB 15; Length 1640;
Best Local Similarity 99.2%; Pred. No. 4.9e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
Db 639 ttctctgcagctggtctttggcatcgagctgagtggaagtggaacccatcgccactgtga 698

QY 96 CATCTTTGCCACCTGCTTGGCCCTCTCTAGCATGGCCTGCTGGTGACAAATCAGATCAT 155
Db 699 catctttgccacctgacctggccctctctactacgatggcctgctgggtgacaatcagatcat 758

QY 156 GCCCA 160
Db 759 gccca 763

RESULT 13
AAQ84116
ID AAQ84116 standard; cDNA to mRNA; 1640 BP.
XX
XX AAQ84116;
XX
XX 08-SEP-1999 (first entry)
XX MAGE-3 gene.
XX Tumour rejection antigen; vaccine; cancer; MAGE-3 gene; ss.
XX Homo sapiens.
XX US5925729-A.
XX
XX 20-JUL-1999.
XX
XX 02-MAY-1994; 94US-0142368.
XX
XX 02-MAY-1994; 94US-0142368.
XX
XX 23-MAY-1991; 91US-0705702.
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PR 09-JUL-1991; 91US-0728838.
 PR 23-SEP-1991; 91US-0764365.
 PR 12-DEC-1991; 91US-0807043.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
 PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;
 XX
 XX WPI; 1999-418294/35.
 XX
 XX New tumour rejection antigen is useful as a vaccine against
 PT cancerous diseases
 XX
 XX Disclosure; Column 51-54; 58pp; English.
 XX
 CC This sequence represents the MAGE-3 gene sequence.
 CC The invention relates to a tumour rejection antigen sequence that is
 CC useful as a tumour rejection antigen for vaccination against cancerous
 CC conditions.
 XX
 XX Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;
 SQ

Query Match 32.9%; Score 74; DB 20; Length 1640;
 Best Local Similarity 99.2%; Pred. No. 4.9e-28;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCGAGCTGCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCAGGTGTA 95
 |||||
 Db 639 ttccttgagctggtctcttgagcatcgagctgagtggaagtggaccccatcggccactgtga 698
 |||||
 QY 96 CATCTTTGCCACCTGCGCTGGCCCTCTCCTACGATGGCCTGCTGGGTGACAAATCAGATCAT 155
 |||||
 Db 699 catcttggccacctgctggcctctctactacgatggcctgctggtgacaatcagatcat 758
 |||||
 QY 156 GCCCA 160
 |||||
 Db 759 gccca 763

RESULT 14
 AAX26974
 ID AAX26974 standard; cDNA; 4204 BP.
 XX
 AC AAX26974;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 DE cDNA encoding MAGE-3 polypeptide.
 XX
 KW MAGE-3 tumour associated gene; human leucocyte antigen Class II;
 KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
 KW osteosarcoma; leukemia; carcinoma; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 2465..3409
 CDS /*tag= a
 FT /*product= "MAGE-3"
 FT
 XX
 XX WO9914326-A1.
 XX
 XX 25-MAR-1999.
 XX
 XX 04-SEP-1998; 98WO-US18601.
 XX
 XX 12-SEP-1997; 97US-0928615.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYVR-) UNIV VRIJE BRUSSEL.
 XX

PI Boon-Falleur T, Chaux P, Corthals J, Heirman C;
 PI Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;
 XX
 XX WPI; 1999-244031/20.
 DR
 DR P-PSDB; AAY01720.
 XX
 XX Isolated peptides that bind to human leucocyte antigen class II
 PT molecules
 XX
 XX Example 5; Page 65-67; 88pp; English.
 XX
 CC The present sequence represents the MAGE-3 tumour associated gene.
 CC Peptides that bind human leucocyte antigen (HLA) Class II molecules
 CC can be derived from the MAGE-3 protein. These peptides and
 CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide
 CC and HLA Class II, are used to treat MAGE-3 related diseases,
 CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
 CC various forms of carcinoma). The peptides are also used to produce
 CC specific antibodies. Detection of the peptides, e.g. in binding
 CC assays, particularly with antibodies, is used for diagnosis of such
 CC diseases.
 XX
 XX Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;
 SQ

Query Match 32.9%; Score 74; DB 20; Length 4204;
 Best Local Similarity 99.2%; Pred. No. 5e-28;
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCGAGCTGCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCAGGTGTA 95
 |||||
 Db 2932 ttccttgagctggtctcttgagcatcgagctgagtggaagtggaccccatcggccactgtga 2991
 |||||
 QY 96 CATCTTTGCCACCTGCGCTGGCCCTCTCCTACGATGGCCTGCTGGGTGACAAATCAGATCAT 155
 |||||
 Db 2992 catcttggccacctgctggcctctctactacgatggcctgctggtgacaatcagatcat 3051
 |||||
 QY 156 GCCCA 160
 |||||
 Db 3052 gccca 3056

RESULT 15
 AAA37927
 ID AAA37927 standard; cDNA; 4204 BP.
 XX
 AC AAA37927;
 XX
 DT 18-AUG-2000 (first entry)
 XX
 DE Human MAGE-A3 nucleotide sequence.
 XX
 KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;
 KW cancer; human; tumour; tumour associated gene product; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200020581-A1.
 XX
 XX 13-APR-2000.
 XX
 XX 15-SEP-1999; 99WO-US21230.
 XX
 XX 05-OCT-1998; 98US-0166448.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYVR-) UNIV VRIJE BRUSSEL.
 XX
 XX Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
 PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;
 PI Heirman C;
 XX
 XX WPI; 2000-317713/27.
 DR

DR P-PSDB; AAB02565.
XX
PT New MAGE-A3 class II binding peptides, useful to diagnose and treat
PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
PT lymphocytes by human leukocyte antigen class II molecules
XX
PS Example 6; Page 96-98; 119pp; English.
XX
CC The present invention relates to MAGE-A3 (tumour associated gene
CC product) human leukocyte antigen (HLA) class II-binding peptides (see
CC AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T
CC cells in the context of HLA class II molecules. The peptides stimulate
CC the activity and proliferation of CD4+ T lymphocytes. The invention also
CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
CC to create antibodies against the MAGE-A3 peptides, the antibodies,
CC peptides and nucleotide sequences can be used to create a vaccine. The
CC peptides are used to diagnose or treat a disorder characterized by
CC expression of MAGE-3, particularly cancer. The methods can also be used
CC in the diagnosis of disorders associated with MAGE-3 expression. Included
CC in the invention are other human tumour antigens (see AAB02596-B02637),
CC and PCR primers used in the course of the invention (see AAA37929-A37937
CC and AAA37941-A37942).
XX
SQ Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;

Query Match 32.9%; Score 74; DB 21; Length 4204;
Best Local Similarity 99.2%; Pred. No. 5e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 36 TTCCTTCGACGTGCTCTTTGGCATCGAGTCGATGGAAGTGGACCCCATCGGCCACGTGTA 95
Db 2932 ttccttcgagctgtcttggcatcgagtcgatggaagtggaccccatcgccacttgta 2991
QY 96 CATCTTTGCCACCTGCCTGGCCCTCTCTACGATGGCTGCTGGGTGACAAATCAGATCAT 155
Db 2992 catcttggccacctgcctggccctctctctacgatggcctgctgggtgacaaatcagatcat 3051
QY 156 GCCCA 160
Db 3052 gccca 3056

Search completed: May 9, 2002, 23:49:42
Job time: 4234 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2002, 21:24:18 ; Search time 1791.78 Seconds
(without alignments)
1694.859 Million cell updates/sec

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Perfect score: 225
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pin:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	69.8	563	10	BG477228
2	157	69.8	768	10	BI086876
3	157	69.8	776	10	BG476912
4	157	69.8	878	10	BG397171
5	157	69.8	886	10	BG76078
6	157	69.8	894	10	BG765817
7	137	60.9	707	10	BG760839
8	137	60.9	876	10	BF792356
9	128	56.9	1021	10	BM470991
10	108	48.0	795	10	BE341476
11	104	46.2	696	10	BE733003
12	102	45.3	704	10	BG764972
13	101	44.9	760	10	BE730893
14	98	43.6	1101	10	BE734462
15	93	41.3	768	10	BG718421
16	93	41.3	929	10	BE275276
17	84	37.3	738	10	BE900916

18	84	37.3	750	10	BE890259	BE890259	601431709
19	84	37.3	1109	10	BG333682	BG333682	602460573
20	83	36.9	683	10	BE407664	BE407664	601299644
21	77	34.2	710	10	BM011988	BM011988	603636402
22	77	34.2	956	10	BE900736	BE900736	601673904
23	74	32.9	623	10	BF793889	BF793889	602255285
24	74	32.9	686	10	BG575715	BG575715	602598794
25	74	32.9	704	10	BI090658	BI090658	602853894
26	74	32.9	769	10	BG765526	BG765526	602739439
27	74	32.9	872	10	BM449726	BM449726	AGENCOURT
28	71	31.6	845	10	BI089076	BI089076	602853444
29	69	30.7	767	10	BI092532	BI092532	602857089
30	68	30.2	803	10	BM015882	BM015882	603642276
31	65	28.9	948	9	AL562721	AL562721	AL562721
32	64	28.4	810	9	AL526639	AL526639	AL526639
33	59	26.2	633	10	BE732114	BE732114	601566119
34	59	26.2	809	10	BI855745	BI855745	603383276
35	56	24.9	845	10	BG481937	BG481937	602526854
36	55	24.4	721	10	BG481226	BG481226	602528552
37	55	24.4	751	10	BE732549	BE732549	601566575
38	55	24.4	816	10	BI086919	BI086919	602850347
39	55	24.4	844	10	BE902106	BE902106	601674881
40	53	23.6	721	10	BM015284	BM015284	603641425
41	52	23.1	740	10	BE727711	BE727711	601564512
42	52	23.1	766	10	BE615115	BE615115	601280487
43	51	22.7	934	10	BG280738	BG280738	602401029
44	50	22.2	597	10	BE281072	BE281072	601157913
45	50	22.2	683	10	BE799994	BE799994	601587723

ALIGNMENTS

RESULT 1

BG477228

LOCUS

DEFINITION

602524237F1 NIH_MGC_20 Homo sapiens

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

563 bp mRNA linear EST 21-MAR-2001
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mRNA sequence.
BG477228
BG477228.1 GI:13409507
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI411 row: i column: 10
High quality sequence stop: 499.
Location/Qualifiers
1. 563
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGG(G). Size-selected >500bp for average
insert size: 1.8kb. Library constructed by Ling Hong in

FEATURES
source

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 133 a 147 c 162 g 121 t

ORIGIN

Query Match 69.8%; Score 157; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 5.3e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
|||||
Db 194 TTCTTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATCGAG 253
|||||
Qy 64 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123
|||||
Db 254 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 313
|||||
Qy 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
|||||
Db 314 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 350
|||||

RESULT 2
BI086876
LOCUS 602850494F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4992143 5',
DEFINITION mRNA sequence.

ACCESSION BI086876
VERSION BI086876.1 GI:14505206
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 768)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L14M1010 row: k column: 24
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FEATURES
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BASE COUNT 170 a 227 c 212 g 158 t 1 others
ORIGIN

Query Match 69.8%; Score 157; DB 10; Length 768;
Best Local Similarity 100.0%; Pred. No. 5.6e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
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|||||
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|||||
Qy 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
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RESULT 3
BG476912
LOCUS 602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5',
DEFINITION mRNA sequence.

ACCESSION BG476912
VERSION BG476912.1 GI:13409178
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 776)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L1CM1412 row: b column: 21
High quality sequence stop: 747.

FEATURES
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BASE COUNT 180 a 197 c 232 g 167 t
ORIGIN

Query Match 69.8%; Score 157; DB 10; Length 776;
Best Local Similarity 100.0%; Pred. No. 5.6e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 64 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123
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RESULT 4
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DEFINITION 602434130F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4552086 5',
mRNA sequence.
ACCESSION BG397171
VERSION BG397171.1 GI:13290619
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: AFCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 197 a 214 c 262 g 205 t
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Qy 64 CTGATGGAAGTGGACCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 123
Db 253 CTGATGGAAGTGGACCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 312

Qy 124 TACGATGGCTGCTGGGTGACAATCAGATCATGCCCA 160
Db 313 TACGATGGCTGCTGGGTGACAATCAGATCATGCCCA 349

RESULT 5
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DEFINITION 60250963F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639670 5',
mRNA sequence.
ACCESSION BG476078
VERSION BG476078.1 GI:13408357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: AFCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1403 row: m column: 15
High quality sequence stop: 730.
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EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/clone_lib="NIH_MGC_84"
 /tissue_type="adrenal cortex carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
 NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
 primed. Average insert size 1.229 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 BASE COUNT 185 a 215 c 248 g 228 t
 ORIGIN

Query Match 60.9%; Score 137; DB 10; Length 876;
 Best Local Similarity 100.0%; Pred. No. 1.1e-59;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CAAGCTTCGATTCCTTGGACGTGGTCTTTGGCATCGAGCTGGAAGTGGACCCCAT 83
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 DB 101 CAAGCTTCGATTCCTTGGACGTGGTCTTTGGCATCGAGCTGGAAGTGGACCCCAT 160
 |||||||
 QY 84 CGGCACGTGTACATCTTTGGCACTGCCTGGGCTCTCTTACGATGGCTGCTGGGTGA 143
 |||||||
 DB 161 CGGCACGTGTACATCTTTGGCACTGCCTGGGCTCTCTTACGATGGCTGCTGGGTGA 220
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 QY 144 CAATCAGATATGCCCA 160
 |||||||
 DB 221 CAATCAGATATGCCCA 237
 |||||||

RESULT 9

BM470991
 LOCUS BM470991 1021 bp mRNA linear EST 05-FEB-2002
 DEFINITION AGENCOURT_6478212 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5562971
 5', mRNA sequence.
 ACCESSION BM470991
 VERSION BM470991.1 GI:18520033
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1021)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1293 row: d column: 12
 High quality sequence stop: 725.
 Location/Qualifiers
 1. 1021

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5562971"
 /clone_lib="NIH_MGC_72"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."
 BASE COUNT 232 a 290 c 292 g 206 t 1 others
 ORIGIN

FEATURES
source

Query Match 56.9%; Score 128; DB 10; Length 1021;
 Best Local Similarity 100.0%; Pred. No. 1.1e-59;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 4.7e-55;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCCTCGATTCTTTCAGCTGCTTTTGGCATCGAG 63
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 DB 596 TTCTTTCTGTGATCTTCAGCAAGCTTCCTCGATTCTTTCAGCTGCTTTTGGCATCGAG 555
 |||||||
 QY 64 CTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 123
 |||||||
 DB 656 CTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 715
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 QY 124 TACGATGG 131
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 DB 716 TACGATGG 723
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RESULT 10
 BE541476
 LOCUS BE541476 795 bp mRNA linear EST 09-AUG-2000
 DEFINITION 601067928F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454135 5',
 mRNA sequence.

ACCESSION BE541476
 VERSION BE541476.1 GI:9770121
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 795)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM8438 row: h column: 08
 High quality sequence stop: 662.
 Location/Qualifiers
 1. 795

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3454135"
 /clone_lib="NIH_MGC_10"
 /cell_line="MGC36"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5 kb. Library prepared by Life
 Technologies."
 BASE COUNT 182 a 199 c 234 g 180 t
 ORIGIN

FEATURES
source

Query Match 48.0%; Score 108; DB 10; Length 795;
 Best Local Similarity 100.0%; Pred. No. 8.5e-45;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCC 112
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 DB 238 TTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCC 297
 |||||||
 QY 113 TGGGCTCTCTTACGATGGCCCTGCTGGGTGACAAATCAGATCATGCCCA 160
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 DB 298 TGGGCTCTCTTACGATGGCCCTGCTGGGTGACAAATCAGATCATGCCCA 345
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RESULT 11

BE733003
LOCUS 601569780F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3844482 5',
DEFINITION mRNA sequence.
ACCESSION BE733003
VERSION BE733003.1 GI:10146995
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 696)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM540 row: P column: 19
High quality sequence stop: 693.
Location/Qualifiers
FEATURES
source
1. 696
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3844482"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." Note: this is a NIH_MGC Library." |"
BASE COUNT 142 a 206 c 204 g 144 t
ORIGIN
Query Match 46.2%; Score 104; DB 10; Length 696;
Best Local Similarity 100.0%; Pred. No. 9.4e-43;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 TTCTTTCGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
Db 560 TTCTTTCGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGAG 619
Qy 64 CTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCAC 107
Db 620 CTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCAC 663
RESULT 12
BG764972
LOCUS 602737745F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4863059 5',
DEFINITION mRNA sequence.
ACCESSION BG764972
VERSION BG764972.1 GI:14075625
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 704)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/Drp
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LCM1724 row: i column: 12
High quality sequence stop: 704.
Location/Qualifiers
FEATURES
source
1. 704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4863059"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." Note: this is a NIH_MGC Library." |"
BASE COUNT 145 a 214 c 200 g 145 t
ORIGIN
Query Match 45.3%; Score 102; DB 10; Length 704;
Best Local Similarity 100.0%; Pred. No. 1e-41;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 55 GGCATCGAGCTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCACCTGCCTG 114
Db 603 GGCATCGAGCTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCACCTGCCTG 662
Qy 115 GGCCTCTCTAGGAGCTGCTGGTGACATCATCATG 156
Db 663 GGCCTCTCTAGGAGCTGCTGGTGACATCATG 704
RESULT 13
BE730893
LOCUS 601570013F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3844707 5',
DEFINITION mRNA sequence.
ACCESSION BE730893
VERSION BE730893.1 GI:10144885
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 760)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM541 row: j column: 04
High quality sequence stop: 742.
Location/Qualifiers

QY	24	CAAAGCTCCGATTCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT	83
D6 <td>649 <td>CAAAGCTTCGATTCTTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT <td>708</td> </td></td>	649 <td>CAAAGCTTCGATTCTTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT <td>708</td> </td>	CAAAGCTTCGATTCTTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT <td>708</td>	708

Qy 84 CGGCCACGTGTACATCTTTGGCACCTGCCTGGG 116
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Db 709 CGGCCACGTGTACATCTTTGGCACCTGCCTGGG 741

Search completed: May 9, 2002, 23:11:17
Job time: 6419 sec

Query Match 100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGCTTTTGGCATC 60
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DB 1 TATTTCCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGCTTTTGGCATC 60
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
|||||
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
|||||
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTCTGATAATC 180
|||||
DB 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTCTGATAATC 180
|||||
QY 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||||
DB 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
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RESULT 2

US-08-299-849B-18
; Sequence 18, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: MAGE-6 gene
US-08-299-849B-18

Query Match 100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TATTTCCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGCTTTTGGCATC 60
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
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DB 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
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QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTCTGATAATC 180
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DB 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTCTGATAATC 180
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QY 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
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DB 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||||

RESULT 3

US-08-142-368A-18
; Sequence 18, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5925729man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.4-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: MAGE-6 gene
; US-08-142-368A-18

Query Match      100.0%; Score 225; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAAAGCTTCGAGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 1 TATTTCTTCTGTGATCTTCAGCAAAAGCTTCGAGATTCCTTGCAGCTGGTCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120

QY 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCCTGATAATC 180
Db 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCCTGATAATC 180

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225

RESULT 4
US-08-967-727-18
; Sequence 18, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: MAGE-6 gene
; US-08-967-727-18

Query Match      100.0%; Score 225; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAAAGCTTCGAGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 1 TATTTCTTCTGTGATCTTCAGCAAAAGCTTCGAGATTCCTTGCAGCTGGTCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120

QY 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCCTGATAATC 180
Db 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCCTGATAATC 180

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225

RESULT 5
US-08-037-230D-18
; Sequence 18, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6235525man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-037-230D-18

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 60
DB 1 TATTTCCTTCGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCTGGGCTC 120
DB 61 GAGCTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCTGGGCTC 120

QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGTGCCAGACAGGCTTCTGATAATC 180
DB 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGTGCCAGACAGGCTTCTGATAATC 180

QY 181 ATCCTGGCCATAATCGCAAGAGGGGACGTGCCCCCTGAGGAG 225
DB 181 ATCCTGGCCATAATCGCAAGAGGGGACGTGCCCCCTGAGGAG 225

RESULT 6
US-09-056-105-7
Sequence 7, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
EARLIER FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 945
TYPE: DNA
ORGANISM: Homo sapiens
US-09-056-105-7

Query Match 69.8%; Score 157; DB 4; Length 945;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTCTGTATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
DB 436 ttcttctctgtatcttcagcaagcttcgattccttcgagctggtctttggcatcgag 495

QY 64 CTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 123
DB 496 ctgatggaagtggaccccatcgccacgtgtacatctttgccacctgctgggctctcc 555

QY 124 TACGATGGCTGCTGGGTGACAATCAGATCATGCCCCA 160
DB 556 tacgatggcctgctgggtgacaatcagatcatgcccc 592

RESULT 7
US-09-056-105-13
Sequence 13, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
EARLIER FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 1019
TYPE: DNA
ORGANISM: Homo sapiens
US-09-056-105-13

Query Match 69.8%; Score 157; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTCTGTATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
DB 501 ttcttctctgtatcttcagcaagcttcgattccttcgagctggtctttggcatcgag 560

QY 64 CTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 123
DB 561 ctgatggaagtggaccccatcgccacgtgtacatctttgccacctgctgggctctcc 620

QY 124 TACGATGGCTGCTGGGTGACAATCAGATCATGCCCCA 160
DB 621 tacgatggcctgctgggtgacaatcagatcatgcccc 657

RESULT 8
US-08-993-738A-2
Sequence 2, Application US/08993738A
Patent No. 5928938
GENERAL INFORMATION:
APPLICANT: van der Bruggen, Pierre; Deplaen Etienne;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Peptides Which Complex With

;; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fulbright & Jaworski L.L.P.
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10022
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;;
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/993,738A
;; FILING DATE: 19-December-1997
;; CLASSIFICATION: 536
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/713,354
;; FILING DATE: 13-September-1996
;; CLASSIFICATION: 536
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 5928938man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1375 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-08-993-738A-2

Query Match 69.8%; Score 157; DB 2; Length 1375;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCCTTGACAGTGGTCTTTGGCATCGAG 63
DB 595 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCCTTGACAGTGGTCTTTGGCATCGAG 654

QY 64 CTGATGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCGTGGGCTCTCC 123
DB 655 CTGATGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCGTGGGCTCTCC 714

QY 124 TACGATGCGCTGCTGGGTGACCAATCAGATCATGCCCA 160
DB 715 TACGATGCGCTGCTGGGTGACCAATCAGATCATGCCCA 751

RESULT 9
US-08-713-354C-2
;; Sequence 2, Application US/08713354C
;; Patent No. 6265215
;; GENERAL INFORMATION:
;; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;
;; APPLICANT: Boon-Falleur, Thierry
;; TITLE OF INVENTION: Isolated Peptides Which Complex With
;; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Felfe & Lynch
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; ZIP: 10022
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/713,354C
;; FILING DATE: 13-September-1996
;; CLASSIFICATION: 536
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6265215man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5460
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1375 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-08-713-354C-2

Query Match 69.8%; Score 157; DB 4; Length 1375;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCCTTGACAGTGGTCTTTGGCATCGAG 63
DB 595 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCCTTGACAGTGGTCTTTGGCATCGAG 654

QY 64 CTGATGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCGTGGGCTCTCC 123
DB 655 CTGATGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCGTGGGCTCTCC 714

QY 124 TACGATGCGCTGCTGGGTGACCAATCAGATCATGCCCA 160
DB 715 TACGATGCGCTGCTGGGTGACCAATCAGATCATGCCCA 751

RESULT 10
US-07-807-043B-11
;; Sequence 11, Application US/07807043B
;; Patent No. 5342774
;; GENERAL INFORMATION:
;; APPLICANT: Boop, Thierry, Van den Eynde, Beno t
;; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
;; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Felfe & Lynch
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; ZIP: 10022
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;;
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/807,043B
;; FILING DATE: 19911212
;; CLASSIFICATION: 424
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; FILING DATE: 9-JULY-1991
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-May-1991

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5342774man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1640 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; FEATURE:
; NAME/KEY: cdna MAGE-3
; US-07-807-043B-11

Query Match 32.9% Score 74; DB 1; Length 1640;
Best Local Similarity 99.2% Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTCTTTGGCATCGAGCTGATGGAAGTGACCCCATCGGCCACGTGTA 95
Db 639 TTCCTTGCAGCTGCTCTTTGGCATCGAGCTGATGGAAGTGACCCCATCGGCCACGTGTA 698

QY 96 CATCTTTGCCACCTGCGCTGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
Db 699 CATCTTTGCCACCTGCGCTGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 758

QY 156 GCCCA 160
Db 759 GCCCA 763

RESULT 11
US-08-299-849B-11
; Sequence 11, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Szkora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
```

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;
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1640 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; FEATURE:
; NAME/KEY: cdna MAGE-3
; US-08-299-849B-11

Query Match 32.9% Score 74; DB 1; Length 1640;
Best Local Similarity 99.2% Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTCTTTGGCATCGAGCTGATGGAAGTGACCCCATCGGCCACGTGTA 95
Db 639 TTCCTTGCAGCTGCTCTTTGGCATCGAGCTGATGGAAGTGACCCCATCGGCCACGTGTA 698

QY 96 CATCTTTGCCACCTGCGCTGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
Db 699 CATCTTTGCCACCTGCGCTGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 758

QY 156 GCCCA 160
Db 759 GCCCA 763

RESULT 12
US-08-142-368A-11
; Sequence 11, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
```


APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3
US-08-142-368A-11

Query Match 32.9%; Score 74; DB 2; Length 1640;
Best Local Similarity 99.2%; Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 95
Db 639 TTCTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 698
QY 96 CATCTTTGCCACCTGCTTGGCGCTCTCTCTAGCATGGCGCTGCTGGTGACAAATCAGATCAT 155
Db 699 CATCTTTGCCACCTGCTTGGCGCTCTCTCTAGCATGGCGCTGCTGGTGACAAATCAGATCAT 758
QY 156 GCCCA 160
Db 759 GCCCA 763

RESULT 13
US-08-967-727-11
Sequence 11, Application US/08967727
Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: Wordperfect
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6025474man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3
US-08-967-727-11

Query Match 32.9%; Score 74; DB 3; Length 1640;
Best Local Similarity 99.2%; Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 36 TTCTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 95
Db 639 TTCTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 698
QY 96 CATCTTTGCCACCTGCTTGGCGCTCTCTCTAGCATGGCGCTGCTGGTGACAAATCAGATCAT 155
Db 699 CATCTTTGCCACCTGCTTGGCGCTCTCTCTAGCATGGCGCTGCTGGTGACAAATCAGATCAT 758
QY 156 GCCCA 160
Db 759 GCCCA 763

RESULT 14
US-08-037-230d-11
Sequence 11, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/037, 230D
;; FILING DATE: 26-MARCH-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/04354
;; FILING DATE: 22-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/807,043
;; FILING DATE: 12-DECEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; FILING DATE: 9-JULY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6235525man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5353
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1640 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA to mRNA
;; FEATURE:
;; NAME/KEY: CDNA MAGE-3
US-08-037-230D-11

Query Match 32.9%; Score 74; DB 4; Length 1640;
Best Local Similarity 99.2%; Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
Db 639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 698
|||||

QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 699 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 758
|||||

QY 156 GCCCA 160
|||||
Db 759 GCCCA 763

RESULT 15
US-08-928-615-1
; Sequence 1, Application US/08928615
; Patent No. 5965535
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.

;; ZIP: 02210-2211
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/928,615
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Van Amsterdam, John R.
;; REGISTRATION NUMBER: 40,212
;; REFERENCE/DOCKET NUMBER: L0461/7017
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-720-3500
;; TELEFAX: 617-720-2441
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4204 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 2465...3406
US-08-928-615-1

Query Match 32.9%; Score 74; DB 2; Length 4204;
Best Local Similarity 99.2%; Pred. No. 5.3e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
Db 2932 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 2991
|||||

QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 2992 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 3051
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QY 156 GCCCA 160
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Db 3052 GCCCA 3056

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